SCORE Search Results Details for Application 10502115 and Search Result 20070517_165827_us-10-502-115-1_copy_17_22.rag.

Score Home Page   Retrieve Application List   SCORE System Overview   SCORE FAQ   Comments / Suggestions

This page gives you Search Results detail for the Application 10502115 and Search Result 20070517_165827_us-10-502-115-1_copy_17_22.rag.

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```
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OM protein - protein search, using sw model

Run on:          May 18, 2007, 23:39:41 ; Search time 212 Seconds
                                         (without alignments)
                                 13.859 Million cell updates/sec


Title:           US-10-502-115-1_COPY_17_22
Perfect score:   29
Sequence:        1 LKKTET 6

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters:      2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_200701:*
                 1:   geneseqp1980s:*
                 2:   geneseqp1990s:*
                 3:   geneseqp2000s:*
                 4:   geneseqp2001s:*
                 5:   geneseqp2002s:*
                 6:   geneseqp2003as:*
                 7:   geneseqp2003bs:*
                 8:   geneseqp2004s:*
                 9:   geneseqp2005s:*
                 10:  geneseqp2006s:*
                 11:  geneseqp2007s:*

    Pred. No. is the number of results predicted by chance to have a
```

<div style="border:1px solid black; padding:1em">

SCORE Search Results Details for Application 10502115 and Search Result 20070517_165827_us-10-502-115-1_copy_17_23.rag.

</div>

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.OM protein - protein search, using sw model

Run on:          May 18, 2007, 23:39:41 ; Search time 247 Seconds
                                          (without alignments)
                                          13.859 Million cell updates/sec

Title:           US-10-502-115-1_COPY_17_23
Perfect score:   34
Sequence:        1 LKKTETQ 7

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters:      2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_200701:*
                 1:   geneseqp1980s:*
                 2:   geneseqp1990s:*
                 3:   geneseqp2000s:*
                 4:   geneseqp2001s:*
                 5:   geneseqp2002s:*
                 6:   geneseqp2003as:*
                 7:   geneseqp2003bs:*
                 8:   geneseqp2004s:*
                 9:   geneseqp2005s:*
                 10:  geneseqp2006s:*
                 11:  geneseqp2007s:*

       Pred. No. is the number of results predicted by chance to have a
```

SCORE Search Results Details for Application 10502115 and Search Result 20070517_165831_us-10-502-115-1_copy_17_22.rup.

This page gives you Search Results detail for the Application 10502115 and Search Result 20070517_165831_us-10-502-115-1_copy_17_22.rup.

```
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OM protein - protein search, using sw model

Run on:        May 18, 2007, 23:41:50 ; Search time 213 Seconds
                                        (without alignments)
                                        30.168 Million cell updates/sec


Title:         US-10-502-115-1_COPY_17_22
Perfect score: 29
Sequence:      1 LKKTET 6

Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters:      3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      UniProt_8.4:*
                1:  uniprot_sprot:*
                2:  uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                              SUMMARIES
                          %
Result          Query
  No.   Score   Match Length DB   ID                      Description
--------------------------------------------------------------------------------
    1     29   100.0     38   2   Q27I67_9HYST            Q27i67 bathyergus
```

SCORE Search Results Details for Application 10502115 and Search Result 20070517_165831_us-10-502-115-1_copy_17_23.rup.

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OM protein - protein search, using sw model

Run on:          May 18, 2007, 23:41:50 ; Search time 249 Seconds
                                            (without alignments)
                                            30.168 Million cell updates/sec

Title:           US-10-502-115-1_COPY_17_23
Perfect score:   34
Sequence:        1 LKKTETQ 7

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters:       3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_8.4:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.
```

<table>
<tr><td colspan="7" align="center">SUMMARIES</td></tr>
<tr><td>Result
No.</td><td>Score</td><td>%
Query
Match</td><td>Length</td><td>DB</td><td>ID</td><td>Description</td></tr>
<tr><td>1</td><td>34</td><td>100.0</td><td>38</td><td>2</td><td>Q27I67_9HYST</td><td>Q27i67 bathyergus</td></tr>
</table>

SCORE Search Results Details for Applicatic

This page gives you Search Results detail for the Application 10502115 and Search Result 2007051

```
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OM protein - protein search, using sw model

Run on:          May 18, 2007, 23:50:00 ; Search time 23 Seconds
                                          (without alignments)
                                 25.527 Million cell updates/sec


Title:           US-10-502-115-1_COPY_17_22
Perfect score:   29
Sequence:        1 LKKTET 6

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:        283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result          Query
   No.   Score  Match Length DB   ID               Description
----------------------------------------------------------------------------
      1     29  100.0     40  2   A59005           thymosin beta - se
      2     29  100.0     40  2   B59005           thymosin beta - sc
      3     29  100.0     41  1   A60290           thymosin beta-9-Me
      4     29  100.0     41  2   B19438           thymosin beta-9 -
      5     29  100.0     43  1   TNBOB4           thymosin beta-4 -
      6     29  100.0     43  2   S21282           thymosin beta-11 -
      7     29  100.0     43  2   S21694           thymosin beta-12 -
```

This page gives you Search Results detail for the Application 10502115 and Search Result 200705]

```
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OM protein - protein search, using sw model

Run on:          May 18, 2007, 23:50:00 ; Search time 26 Seconds
                                            (without alignments)
                                         25.527 Million cell updates/sec

Title:           US-10-502-115-1_COPY_17_23
Perfect score:   34
Sequence:        1 LKKTETQ 7

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:      283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	100.0	40	2	A59005	thymosin beta - se
2	34	100.0	41	1	A60290	thymosin beta-9-Me
3	34	100.0	41	2	B19438	thymosin beta-9 -
4	34	100.0	43	1	TNBOB4	thymosin beta-4 -
5	34	100.0	43	2	S21282	thymosin beta-11 -
6	34	100.0	43	2	S21694	thymosin beta-12 -
7	34	100.0	44	1	A38682	thymosin beta-4 [v

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```
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OM protein - protein search, using sw model

Run on:         May 18, 2007, 23:57:45 ; Search time 34 Seconds
                                        (without alignments)
                                        15.377 Million cell updates/sec


Title:        US-10-502-115-1_COPY_17_22
Perfect score: 29
Sequence:     1 LKKTET 6

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:      650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:       650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Issued_Patents_AA:*
              1:  /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
              2:  /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
              3:  /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
              4:  /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
              5:  /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
              6:  /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
              7:  /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                              SUMMARIES
```

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```
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OM protein - protein search, using sw model

Run on:          May 18, 2007, 23:57:45 ; Search time 40 Seconds
                                          (without alignments)
                                          15.377 Million cell updates/sec

Title:           US-10-502-115-1_COPY_17_23
Perfect score:   34
Sequence:        1 LKKTETQ 7

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:      650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
             1:  /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
             2:  /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
             3:  /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
             4:  /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
             5:  /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
             6:  /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
             7:  /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                            SUMMARIES
```

SCORE Search Results Details for Application 10502115 and Search Result 20070517_165842_us-10-502-115-1_copy_17_22.rapbm.

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```
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OM protein - protein search, using sw model

Run on:          May 18, 2007, 23:58:26 ; Search time 121 Seconds
                                          (without alignments)
                                          22.984 Million cell updates/sec


Title:           US-10-502-115-1_COPY_17_22
Perfect score:   29
Sequence:        1 LKKTET 6

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:      2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_AA_Main:*
          1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
          2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
          3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
          4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
          5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
          6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                          SUMMARIES
              %
```

SCORE Search Results Details for Application 10502115 and Search Result 20070517_165842_us-10-502-115-1_copy_17_23.rapbm.

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OM protein - protein search, using sw model

Run on:         May 18, 2007, 23:58:26 ; Search time 141 Seconds
                                        (without alignments)
                                        22.984 Million cell updates/sec


Title:          US-10-502-115-1_COPY_17_23
Perfect score:  34
Sequence:       1 LKKTETQ 7

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters:    2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_AA_Main:*
          1:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
          2:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
          3:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
          4:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
          5:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
          6:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                              SUMMARIES
            %
```

SCORE Search Results Details for Application 10502115 and Search Result 20070517_165846_us-10-502-115-1_copy_17_22.rapbn.

<u>Score Home Page</u> <u>Retrieve Application List</u> <u>SCORE System Overview</u> <u>SCORE FAQ</u> <u>Comments / Suggestions</u>

This page gives you Search Results detail for the Application 10502115 and Search Result 20070517_165846_us-10-502-115-1_copy_17_22.rapbn.

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```
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OM protein - protein search, using sw model

Run on:         May 18, 2007, 23:59:47 ; Search time 82 Seconds
                                        (without alignments)
                                        22.857 Million cell updates/sec

Title:          US-10-502-115-1_COPY_17_22
Perfect score:  29
Sequence:       1 LKKTET 6

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1301799 seqs, 311203995 residues

Total number of hits satisfying chosen parameters:      1301799

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_AA_New:*
          1:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
          2:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
          3:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
          4:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
          5:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
          6:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
          7:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
          8:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.
```

SCORE Search Results Details for Application 10502115 and Search Result 20070517_165846_us-10-502-115-1_copy_17_23.rapbn.

This page gives you Search Results detail for the Application 10502115 and Search Result 20070517_165846_us-10-502-115-1_copy_17_23.rapbn.

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OM protein - protein search, using sw model

Run on:         May 18, 2007, 23:59:47 ; Search time 95 Seconds
                                         (without alignments)
                                         22.857 Million cell updates/sec


Title:          US-10-502-115-1_COPY_17_23
Perfect score:  34
Sequence:       1 LKKTETQ 7

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       1301799 seqs, 311203995 residues

Total number of hits satisfying chosen parameters:     1301799

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Published_Applications_AA_New:*
          1:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
          2:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
          3:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
          4:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
          5:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
          6:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
          7:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
          8:    /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.
```